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GenCore version 5.11.3
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OM protein - protein search, using sw model

Run on.

January 16, 2063, 16,39.12 , Scarch time 17,4857 Seconds (without alignments) 28.464 Million cell updates/sec

US-09-856-070-21 60 1 BELMIRLQDYEE 12 Title: Perfect score: Sedneuce:

Scoring table:

BLOSUM62 Gapop 10 0 , Gapext 0 5

Total number of hits satisfying chosen parameters:

112892 scgs, 41476328 residues

Scarched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing lirst 45 summaries

SwissProt_40:* Database :

Prod No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	BOVIN P31976 bos taurus	HUMAN P15311	F26040 1	S01.AC 033600	HITMAN P220R3	PYRAB QQurc8		P37599	HUMAN	_METUA Q58718 :	AN	RAT	CHICK P0775	HIMAN	_SCHPO Q9uti6	BACSU	HIMAN	_PAT	SCHPO ONDROZ		YEAST \$05024	P40047	Z. C	P26042	HUMAN	- MOUSE	LPIG P26044 sus scrofa	BBS2_HUMAN Q9bxc9 home sapien	93M060		T PYRAB
•	DB ID	1 EZPI	1 F7R	1 FEER	1 KA50	1 FriT	1 PASA	1 RRS	1 CHEV	1 555	1 RA50	1 SPCN	1 SPCI	1 SPCN_(1 HI 1:1	1 FCT1	1 pP91	1 AACT	1 ^^^1.	1 URPB	1 1,0001	, VM7	1 DHA5_	1 MOES	1 MOE	1 RAD]	I RADI	1 RADI.	1 BBS	1 BBS.	1 BBS	CVV
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* Ouery	Match	100 0	100 0	95.0	73.3	65.0	65.0	63	61.7	•	61.7				60 n	60 0	0 09	0 09	U 09	0.09	59.2	58.3	58.3	58.3	58 80	58.3	5,9	58.3	58.3	58.3	ι. α	ر در در
	Score	9	9	57	44	39	30	38	37	37	3.7	37	3.7	37	36	36	36	36	36	36	35.5	35	35	35	32	35	3.5	35	35	35	ੂ ਦ∙ ~-	en m
Result	NO.	-	CI	m	4	Ŋ	٤	7	80	5	10	11	12	13	14	15	16	17	18	19	20	ç.	25	23	7.	25	26	27	28	53	30	31

4	35	58.3	4473	_	PLE1 CRIGR	094i55 cricetulus
ı,	35	58.3	4684	_	PLET HUMAN	O15149 homo sapien
99	35	58.3	4687	٦	PLE1_RAT	P30427 rattus norv
17	34.5	57.5	554	Н	CSF1_HUMAN	P09603 homo sapien
38	34	56.7	126	7	HAP1_HUMAN	P54255 homo sapien
68	34	56.7	199		COAE_CLOPE	O8xix0 clostridium
01	34	56.7	3 Ū B	, .	YN8G_YEAST	P53728 saccharomyc
,	. Y	56.7	315		Y ZOS AQUAE	Obb403 aguitex aeo
24	34	56.7	332	-1	KC2A_MAIZE	F28523 sea mays (m
<u>~</u>	34	56.7	333	~	KC21_ARATH	008467 arabidopsis
4	34	56.7	333	Н	KC22_ARATH	Q08466 arabidopsis
Ľ)	34	56.7	333		KC23_ARATH	064817 arabidopsis

ALIGNMENTS

F31976: 01-JUL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last sequence un 16 OCT 2001 (Rel. 40, Last sequence un 16 OCT 2001 (Rel.) (Villin 2) Bos taurns (Bovinae) Eukaryota; Metazoa; Chordata; Craniat Mammalia; Eutheria; Cetartiodactyla; Hovidae; Bos taurns (Bovinae; Bos Transucheria; Cetartiodactyla; NCHILTAXID-9913; Lastine Hos. NCHILTAXID-9913; Lastine Hos. TISSUE-Brain; Zhao Ho, Saijoh K., Dum Ferrin and obsteomettin, two proteins growth, are enriched in the locus coemon; Cell. Neurosci. 4:64-73(1993). SEQUENCE FROM N.A. TISSUE-Ridher, Lastine Locus (Lel.) (Rel.) (Rel.	KEST LERI	
	2 5	EZRI_BOVIN STANDARD; PRT; 580 AA. Paidze:
) Id	
	5 E E	
	. .	
	SO	Bos taurus (Bovine).
	3 8	Eukaryota, Metazda, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia: Eutheria: Cetartiodactvia: Ruminantia: Pecora: Rovoidea:
	3	Hovidae; Bovinge; Bos.
	× ×	NCB1_Tax1D≈9913; [1]
	RP	SEQUENCE FROM N.A.
	Z A	IISSUE-Brain; Bergson C.M., Zhao H., Salioh K., Duman P.S., Nestler F.T.
	Z.	"Earlin and osteonectin, two proteins associated with cell shape and
	<u>x</u>	growth, are enriched in the locus coeruleus.";
	_ Z	Mol. Cell. Neurosci. 4:64-73(1993). [2]
	RP	SEQUENCE OF 1-15 AND 126-140.
	Ca.	TISSUE-Kidney:
	X 5	MEDLINE-96239137; PubMed-8660651;
	Ç [datac A., delbod M.C., boucc F., Miviere S.) "Proteins and their amine acid compositions: uniqueness, variability,
	۵. ن	and applications ";
	₹ :	AFON RIOCHDOM, BIOPRYS, 340,229-23/(1996), PREMITTIAN PROBABLY INVERSEL IN CONNECTIONS OF MATERIAL AVEOLOGYPTERAL
	50	STRUCTURES TO THE PLASMA MEMBRANE.
	ر د د	-1 - SCHC'ELLULAR LONALION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN
	3 5	(CYTOPLASMIC SIDE). PIM - PHOSPHORYLATED BY PROTEIN-TYPOGINE KINASES.
	22	-! SIMILARITY: CONTAINS 1 BAND 4.1 LIKE DOMAIN.
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	. و	TOTAL SWINGSTROTT CONTY, 18 COPYTIGHT. IT IN PICCUSCO LITTLEFY A COLLEGIOR FORMER THE DWINE INSTITUTE OF BIOLOGOXMATICS, and the DWINE CONTESTATION
	CC	the European Bioinformatics Institute. There are no restrictions on i
	<u>:</u>	use by non-profit institutions as long as its content is in no w
	88	modified and this statement is not removed. Goade by and for commerci- notities requires a linease consequent escaphing commerces on only observed
	9	of send an email to license@isb-sib.ch).
	CC	
	DR.	EMBL; M98498; AAA30510.1;
	ai a Galo	InterProj IPR690299; Band_4.1.
	DR	Proceeding Francis of Editory and Editory Processing Pr
	33	Pfam, PF00769; ERM; 1.
	3	PRINTS: PR00935; HAND41.
	3 C	SMART, SM00295; B41; 1:
	d C	FRASITE, PSOUGGO; BAND_41_1; 1.
	12	PROSITE; PS50057; BAND_41_3; 1.
	X	Structural critical Octobroton Phosphorylation

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pakkanon P., Grzeschik K.-H., Wahlstroom I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Egerton M., Moritz R.L., Druker B., Kelso A., Simpson R.J.;
"Identilication of the 70kD heat shock cognate profein (Hsc70) and
alpha-actinin-1 as novel phosphotyrosine-containing proteins in T
lymphorytes.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo Sapiens (Human).
Eukaryota; Metasoa: Chordata; Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Krieq J., Hunter T.,
"Identification of the two major epidermal growth factor-induced tyrosine phosphorylation sites in the microvillar core protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Offenwaelder B., obermaler B., Mewes H.-W., Weil B., Wlemann S.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cytovillin, a microvillar Mr 75,000 protein. cDNA sequence, prokaryotic expression, and chromosomal localization."; J. Biol. Chem. 264:16727 16732(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gould K.L., Bretscher A., Esch F.S., Hunter T.; "cDNA cloning and sequencing of the protein-tyrosine kinase substrate errin, reveals homology to band 4 ! ";
                                                                                                                                                                                                                                                                                                                            100.0%; Score 60; DB 1; Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; indels
                                           PHOSPHORYLATION (BY PDGFR) (BY SIMILARITY).
                                                                                                                                        PHOSPHORYLATION (BY PDGFR)
                                                                                                                                                                                                                               ECD563E5C200FAA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys Pos Commun 224:666-674(1996)
                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EZRI_HUMAN STANDARD; PPT; 585 AA. P15311; P25714; Q9NSJ4; QNNSJ4; QNNS
                                                                                                                                                                                        (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
BAND 4.1 LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hiol. Chem. 267:19258-19265(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ezrin (p81) (cytovillin) (Villin 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90076135; PubMed-2591471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89380299; PubMcd-2674140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96311348; PubMed-8713105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORPLATION BY POGFR.
MEDLINE-92406868; Pubmed-1382070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92388649; PubMed-1381389;
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                                                                                                                                                                                                                                         58524 MW:
                                                                                                                                                                                                                                                                                                                                                                            100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 8:4133-4142(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EELMURLODYEE 12
                                                                                                                                                                                                                                    580 AA;
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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J. Immunol. 14
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                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                            Query Match
                                                MOD_RES
                                                                                                                                        MODERES
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EZRI_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL STRUCTURES TO THE PLASMA MEMBRANE. SURCEILLURAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Funayama N., Nagaluchi A., Salo N., Tsukila S., Tsukila S.; "Radixin is a novel member of the band 4.1 family."; J. Cell Biol. 115:1039-1048(199).
-i- Function: Probabily involved in Connections OF Major CytoSkeletal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metacoa, Chordata, Craniata, Vertebrata, Esteleostomi:
Mammalia, Eutheria, Kodentia, Sciurognathi, Muridae, Murinae, Mus
                                                (CYTOPLASMIC SIBE).
-!- TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 60; DB 1; Length 585; 100.0%; Pred. No. 0.0027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (BY PDGFR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZAB44D140E4H06CC CRC64;
                                                                                                 PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PS00660; BAND_41_1; 1.
PROSITE: PS00661; BAND_41_2; 1.
PROSITE: PS0057; BAND_41_2; 1.
Structural protein, Cytoskeleton, Phosphorylation.
INIT_MET 57 224 BAND 4.1-LIKE.
                                                                                                                   SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1992 (Rel. 22, Greated)
01-MAY 1992 (Rel. 22, East scquence update)
16-OCT-2001 (Rel. 40, East annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            585 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURES TO THE PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                               EMBL; AL162086; CAB82418.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hzrin (p81) (Cytovillin) (Villin 2).
                                                                                                                                                                                                                                                                                                                                                                                                                             LuterPro: IFR000798; Lz/rad/moesin.
Pfam; PF00373; Band_41; 1.
                                                                                                                                                                                                                                                              EMBL; X51521; CAA35893.1; -. TAT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-92064635; Pubmed-1955455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPR000299; Band_4.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69267 MW;
                                                                                                                                                                                                                                                                                                                                                               SWISS-2DPAGE; P15311; HUMAN.
Genew; HGNC:12691; VIL2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00935; BAND41.
SMART; SM00295; B41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00769; ERM; 1,
                                                                                  EPITHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 EELMLRLQDYEE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RELMIRICONYEE 12
                                                                                                                                                                                                                                                                                                                               PIR; S09263; S09263.
PIR; A34400; A34400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         531 5
585 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCB1_Tax ID=10090;
                                                                                                                                                                                                                                                                                                                                                                                           MIM; 123900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EZRI_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation for Extractions on its use by non-profit institutions and is also only as its content is in no way modified and this statement is not removed "Rappe by and for commencial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elie C., Baucher M.F., Fondrat C., Forterre P.;
"A protein related to everyal and batterial iMA-motor proteins in the Typerthermophilic archaeon Sulfolobus acidocaldarius ": I Mol Evol 45:107-114(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             construction involved in page solution of the result of the red of the result of the r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Involved in DNA double strand break repair (DSRP) The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea, Ctenatchaeota, ThetMoptotel, Suifolobaies, Sulfolobaeee;
Sulfolobus.
-!- TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repositioning DNA ends into the mrell active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
-!- SUBUNIT: Forms a complex with mrell (By similarity).
-!- SIMILARITY: HELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (BY PDGFR)
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2057RDR2B2B005D2 CRC64,
                                                                          PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES. SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57, PB 1;
Pred. No. 0.0092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Ref. 40 last sequence update)
16-OCT-2001 (Ref. 40, last annotation update)
DNA double-strand break repair rad50 AIPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY
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STRAIN-ATCC 33909 / NYIR 11770 / DSM 639;
MEDLINE-97362314; PubMed-9211741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to licensealsb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPROO0798; P7/rad/moesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART: SM00295; B41; 1.
PPOSITE: PS00660: BAND_41_1; 1.
PROSITE: PS00661: HAND_41_2; 1.
PROSITE: PS00651: HAND_41_2; 1.
SKTUCTUTAL PROTEIN: CYTOSKELETON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Inst smp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR000299, Band_4.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       585 AA; 69214 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMHL: X60671; CAA43086.1; -.
PIR; B41129; B41129.
MGD: MGT:98931; Vil2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PF00373, Band_41; 1.
Pfam; PF00769; FRM; 1
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9.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00935; BAND41.
SMART; SM00295; B41; 1.
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                                                EPITHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EELMLRLQDYEE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCB1_TavID=2285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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SOLUTION NEW TONE NEW
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                                                                                               entities requires a incense agreement (See http://www.isb-sib.ch/announce/or send an email to incense@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Peripheral blood leukocytes;
MEDLINE-G1373770, PhDMed 1716/30;
Lowe J.B., Kukowska-Latallo J.F., Nair R.P., Larsen R.D., Marks R.M.,
Macher B.A., Kolly R.J., Brist L.K.;
"Macher B.A., Robing of a funda: fucksyltransferase yenc that determines expression of the Lowis x and ViM-2 epitopes but not ELAM-1-dependent
                                                                                                                                                                                                                                                                                                                                                                                     Gaps

    Bibl. Chem. 266:21777-21783(1991).
    FUNCTION: MAY CATALYSE ALPHA-1, 3 GLYCOSIDIC LINKAGES INVOLVED IN
THE EXPRESSION OF LEWIS X/SSEA-1 AND VIM-2 ANTIGENS.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kumar R., Potvin B., Muller W.A., Stanley P.,
"Cloning of a human alpha(1,3) fucosyltransferase gene that encodes
EIFT but does not confer ELAM-1 recognition on Chinese hamster ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Codit S.F., Hossion C., Soff D., Griffiths B., Fizard R., Newman B.,
Chi-Rosso G., Lobb R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C1 UCT:1996 (Nel. 34, Last sequence update)
L57UN-2002 (Rel. 41, Last annotablen update)
Aigha-(1.2)-furosyltransferase (E) E.4.1...) (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase 4) (FUCT-IV) (ELAM-1 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN, MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazua; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "ELFT: a gene that directs the expression of an ELAM-1 ligand.";
                                                                                                                                                                                                                                                                                                                                                                                   Ġ
                                                                                                                                                                                                                                                                                                                                           73.3%; Score 44; DH 1; Length 886; 66.7%; Pred. No. 3.2; alive 3, Mishatches 1, Indels
                                                                                                                                                                                Interpro; IPPU0.5557, 1.
Probon: P000006; AMC_transportr: 1.
DNA repair; Hydrolase; AIP-binding; Coiled coil.
NP_BIND 30 37 AIP (BY SIMILARITY).
NP_BIND 174 727 COILED COIL (POTENTIAL).
'54857 MW; 0590AE1403194104 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          405 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chem. 266:17467-17477(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            celi transfectants.";
J. Biol. Chem. 266:21777-21783(1991).
                                                                                                                                                     EMBL: Y10687; CAA71688.1; -.
InterFro, 18E003439, AbC_transportr.
InterPro; 18E003395; SMC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORM IN TRANS CISTEPNAE OF COLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-92042084; PubMed-1718983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1991 (Rel. 19, Created)
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Hest Local Similarity 65.70
1.3 8. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD:
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                                                                                                                                                                                                                                                                                                                                                                                                                         1 EELMLRLODYEE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fucosyltransferase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell adhesion."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUI4 OR FLFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUT4_HUMAN
P22083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUT4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
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-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-1999) to the EMRLAGENBARK/TORK databases
FINCTION: Involved in DNA double-strand break repair (DSHP)—The
radSubmic1 complex possesses single-strand endonuclease activity
and ATP dependent double-strand-specific exenuclease activity.
RadSU provides an ATP-dependent control of mrelt by unwinding
aud/or repositioning DNA ends into the mrelt active site (By
                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaca, Euryarchacota, Thermococci, Thermococcales, Thermococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        IUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·.
                                                                                                                                                                                                                                                                                                                Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Forms a complex with meell (By similarity).
SIMILARITY: HELONGS TO THE SMC PAMILY, KADSO SUBHAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.0%; Score 39; DB 1; Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             P -> R (IN REF. 2 AND 3).
E -> D (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DE72E1FP4390268p cP44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA double-strand break repair rad50 Arpase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     880 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2: Mismathhos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bred No.
                                                                                                                                                              EMBL; M58596; AAA63172.1; -.
EMBL; M58597; AAA63173.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRI;
                                                                                                                                                                                                                                                                                              Pfam; PF00852; Glyco_transf_l0; l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45569 MW;
                                                                                                                                             EMBL; M65030; AAA92977.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F. F. 78.
                                                                                                                                                                                                                                                                         InterPro; IPR001503; GT_10.
                                                                                                                                                                                                                                                                                                                                     Signal-anchor; Golgi stack.
                                                                                                                                                                                                     S65161; AAB20349.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              structure and evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                         Genew; HGNC:4015; FUT4.
                                                                                                                                                                                                                                                                                                                                                                     43
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87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FELMLRLQDYEE 12
                                                                                                                                                                                                                        PIR; A36340; A35340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
405 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-GES / Orsay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RADSO OR PAR0812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
                                                                                                                                                                                                                                                        104230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KA50_PYRAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrocoeus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21181710; PubMed 11285352;
Nishimura D.Y., Searby C.C., Carmi R., Elbedour K., Van Maldorqem I., Fullon A.H., Lam B.L., Powell B.R., Swiderski K.E., Hudge K.E., Haider N.H., Kwitek-Black A.E., Ying I., Dubl D.M., Gorman S.M., Heon E., Iannaccone A., Bonneau D., Bieserker L.G., Jacobson S.G., Stone E.M., Sheffield V.C.;
Postlional Cloning of a novel gene on chromosome 16q causing Bardet Biedl syndrome (BBS2).";
Hum. Mol. Genet 10:865-874(2001).
                                                                                                                                                                                                                                                                                                                                                                 Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebralish) (Danio rerio).
Eukaryota, Metazoa; Chordata; Craniala; Verfebrata; Eufeleostomi;
Actinoptorygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                            DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete profeome.
NP BIND 30 37 ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                   0:
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C
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                                                                                                                                                                                                                                                                                                                     65.0%; Score 39; DB 1; Length 880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                            NP BIND 30 37 ATP (BY SIMILARITY).
DOMAIN 144 745 COLLED COLL (PATENTIAL).
SEQUENCE 880 AA: 103970 MM; FDB177EC7E026479 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326770AC45H36M90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 AA.
                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                         Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mardet Bied! Syndrome 2 protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                         EMBL: AJ248286; CABS0131.1; -.
Interpro: IPPROMSSES, AAA_ATPASE.
interPro: IPR004339; ARC_transportr.
interPro: IPR003395; SMC_N.
                                                                                                                                                                  ProDom; PD000006; ABC_transportr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -JUN-2002 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                                                             66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF342739; AAK28555.1;
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 66.79
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                        SMART; SM00382; AAA; 1.
                                                                                                                                                SMC_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                               589 EELNLRIQELEE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 QNLMLELRNYEE 357
                                                                                                                                                                                                                                                                                                                                                                                                         1 RELMIRIQUYEE 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       715 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCB1_Tax1D=7955;
                                                                                                                                              Pfam; PP02463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BBS2_BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHEV_BACSU
                                                                                                                                                                                                                                                                                                                     Query Match
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-!- PIM: PHOSPHORYLATED BY CHEA (POTENTIAL).

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A MILLINE THOUGH TO THE MAN TO THE MAN ALLONG G.,

RA Aceved V. Rentero M.G. Bessieres P. Bolotin A. Horchert S.

RA Bourise R., Houseld C.V., Caldwell H., Capudon V., Canter N.M.,

RA Bourise R., Houseld C.V., Caldwell H., Capudon V., Canter N.M.,

RA Brouiliet S., Ernachi C.V., Caldwell H., Capudon V., Daniel R.A.,

RA Choi S.K., Codani J. J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Chim S.K., Calager P., Coffeau A., Colightly R. J., Calders N.,

RA Chim S.Y., Claser P., Coffeau A., Colightly R. J., Calders N.,

RA Ghims J.Y., Claser P., Coffeau A., Colightly R. J., Crandi G.,

RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Hibert B., Raramata D., Kasahara Y., Klain C.,

RA Kucha K., Lapidus A., Laddinois S., Lauber J., Lazarevic V.,

RA Kobayashi Y. Knetter P., Mizuno M., Mosstl D., Nakai S., Rundon M.,

RA Hort B., Mallado R.P., Mizuno M., Mosstl D., Nakai S., Noback M.,

RA Hersecan E., Pujir P., Portelelle D., Pormollik S., Perscott A.M.,

RA Persecan E., Pujir P., Puraelle P., Papropoil G., Peymolds S.,

RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Schin H.S., Scolfone F.,

RA Takeuchi M., Tamakoshi A., Taragi T., Takahashi H., Takomaru K.,

RA Takeuchi M., Tamakoshi A., Taragi T., Takahashi H., Takomaru K.,

RA Takau A., Wanbultt R., Wedler E., Wedler F., Vasaurott A.,

RA Takau A., Wanbultt R., Wedler E., Wedler F., Vasaurott A.,

RA Takau A., Wanbultt R., Wedler E., Wedler H., Welkzenegger T.,

RA Winters P., Winbulk H.F., Zundenbol M., Vasuniote K., Yasuniote K., Yatu A.,

RA Yoshikawa H.F., Zundenbol H., Vasuniote K., Yasuniote Genome sequence of the Gram-positive bacterium Hacilius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosario M.M.L., Fredrick K.L., Ordal G.W., Helmann J.D., redundant Chemotaxis in Bacillus subtilis requires either of two functionally redundant Chem homologs." "The Rorrerical Pre-2784 2784 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXCITATION AND A METHYLATION-DEPENDENT ADAPTATION. CHEW AND CHEM FUNCTION TOGETHER TO COUPEE GHEM ACTIVATION TO METHYL-ACCEPTING CHEMOTAXIS PROTEIN RECEPTOR STATIS AND POSSIBLE CHEM-DEPENDENT PHOSPHORYLATION OF CHEV CONTRIBUTES TO ADAPTATION
                                                                                                                                                                                                                                                                                                    Theal chemetaxis signating pathways in Bacillus subtilis: a sigma D-dependent gene enrydes a novel protein with both theM and theY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: PEAK EXPRESSION IS SEEN IN FARLY STATIONARY
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-1- FUNCTION: CHEMOTAXIS INVOLVES BOTH A PHOSPHORYLATION-DEPENDENT
                                                                                                                                                Firmicutes, Bacillales, Bacillaceae, Bacillus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1997) to the EMEL/GenBank/DDBT databases
             01-001-1994 (Rel. 30, Greated)
01-001-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Pel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                  Bacteriol, 176:2727-2735(1994).
                                                                                                                                                                                                                                                          MEDILINE-94222854; PubMcd-8169223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDITINE GRO44033; PubMod G484377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94222855; PubMed-P" 49224
                                                                                                                                                                                                                                                                                 Predrick K.L., Helmann J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scanlan E., Devine K.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 390-249-256 (1997)
                                                                                  Chemotaxis protein cheV.
                                                                                                                                                                                                                                                                                                                                                  homologous domains."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                            Bacillus subtilis.
                                                                                                                                                                     NCBI_TaxID-1423;
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                                                                                                                                                   Hacteria;
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                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
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14 - 153 - CHEW.
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EGHURASI1451C4L)18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Frekeris E., Savies J.M., Scheller R.H.; "Identification of a novel Rabl1/25 binding domain present in eterin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Prediction of the coding sequences of unidentified human genes, X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; PNA Pes. 5:16e-176(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo Sapiens (Human).
Eukaryota; Metuzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
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mura N., Ohara O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.7%, Score 37, DB 1, Length 303, 58.3%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2, Indels
                        -!- SIMILARITY: CONTAINS 1 CHEW DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PESPONSE PEGULATOPY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           075154: Q9N010: Q9H1GO: Q9H155;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS50110; RESPONSE_REGULATORY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chem. 276:38966-38970(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Subtilist, BG10823; chev.
InterPro; IPK002545; Chew.
InterPro; IPK001789; Response_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21486406; PubMed-11481332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probom; PD000039; Posponse_reg; 1.
SMART: SM00260; CheW: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98403880; PubMed-9734811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piam; PF00072; response_reg; 1.
                                                                                                                                                                                                                                                                                                                                                                                             EMBE, AJEES87; CAA10864.1; -.
EMBE, 299111; CAB13274.1; -.
PIR, S41419; S41419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 AA; 34633 MW;
                                                                                                                                                                                                                                                                                                                                         EMBL, 229584, CAA82701.1; -. EMBL, 005345; AAA16526.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plam; PF01584; CheW; 1.
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Best Local Similarity
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J. Bicl. Chem. 27
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TISSUE-Lund;
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                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Broinformatics and the EMBL outstation-the Burpagen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/dannounce/or send an email to license@isb-sib.ch).
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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Hake T.A., Errecraid T.M., Clayten P.A., Gosayne J.D.,
Kerlavage A.R., Dougherty B.A., Iomb J.-F., Adams M.D., Reich C.L.,
Overbeek R., Kirkness E.F., Weinstenk K.C., Merrick J.M., Glodek A.,
Scott J.L., Geodhagen N.S.M., Weidmann T.F., Fuhrmann T.L., Nguyen D.,
Ultreback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Banna M.C.,
Cotton M.D., Roberts K.M., Burst, M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.G., Worse C.R., Venter J.C.,
Complete genome sequence of the methanogenia archaecen, Methanococcus
                                                           "Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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            Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
Tutarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                   -!- SIMILARITY: CONTAINS 2 EF HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.7%; Score 47; DB 1; Length 756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                     Wallis J., Lloyd C., Hall R.;
Submitted (NOV-2000) to the DMBL/ScanBank/EDBJ databases.
-!- SUBUNIT: Binds to RABII and RAB25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264CHT399F28AFB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchaeota; Methanococci, Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EF HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
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40, Tast annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : : :
                                                                                           Hum. Mol. Genet. 10:339-352(2001).
MEDLINE-21096910; PubMed 11157797;
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16-OCT-2001 (Pel. 40, Last sequ
                                                                                                                                                                                                                                                                                                                                   EMBL; AF195731; AAL12940.1; -
EMBL; AB014565; BAA31640.1; -
                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE006463; AAK61232.1; -. EMBL; AL023881; CAB92745.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82439 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: AL049542; CAC17519.1; -
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InterPro; IPR002048; EF-hand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Calcium binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         756 AA;
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tes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAD50 OR MJ1322.
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                                           Hidds D.R.;
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O
rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding and/or repositioning DNA ends into the mrell active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               moon in the product of the noncrythroid spectrins. Multiple polypeptides are predicted by sequence analysis of cDMAs encompassing the coding region of human noncrythroid alpha-spectrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probon: PD0000065, ABC_transportr; 1.
DNA repair, Hydrolase, ATP binding; Coiled coil; Complete proteome.
NP_BIND 32 39 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Erkarjuda, Metudda, Cholduda, Craniata, Veltebrata, Enteleostomi;
Mammalia; Euthoria, Primates, Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE Fetal brain; Cancillary 1.0. State of human alpha 11 fetal brain spectrin."; Complete cDNA sequence of human alpha 11 fetal brain spectrin."; Submitted (FEB-1997) to the EMBL/GenBauk/DDEJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U13815; U16606; U9F0V0; U13186;
U1-NOV-1997 (Rel. 35, Last. sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2004 (Rel. 41, Last annotation update)
Spectrin alpha chain, brain (Spectrin, non-crythroid alpha chain)
(Alpha II spectrin) (Fudrin alpha chain).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.7%; Score 37; DB 1; Length 1005;
                                                                                                                                               SIMILARITY: BELONGS TO THE SMC FAMILY, RAD50 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 COLLED COLL (POTENTIAL).
119387 MW; 9BBBB48173E78BF3 CRC64;
                                                                                                                         SUBUNIT: Forms a complex with mrell (By similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003439; ABC_transportr.
IPR003405; SMC_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90170948; Pubmed-2307671;
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                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U67572; AAB99331.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1PR003395; SMC_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                648
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Pfam; PF02483; SMC_C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1005 AA;
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                                                                                          similarity).
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                                                                                                                                                                                                                                                                                                                                                   MITAKAMI N., Speed W.C., Scandan M.I., Zychowski P.L., Worterborg L., Pakstis A.J., Kidd J.P., Kidd K.K.;

"Association and linkape analyses of the innerythroid alpha-spectric (SPTANI) gene on chromosome 9G34 with a large Swedish kindred.";

Submitted (MAY-1999) to the EMBL/GenBank/ThDRI databases

-!- FUNCTION: FOHPHIN, WHICH SERMS TO ME INVOLVED IN SECRETION, INTERACTS WITH CAIMONULIN IN A CALCIUM-DEPENDENT MANNEP AND IS THUS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE CALCIUM-DEPENDENT MOVEMENT OF THE CALCIUM-DEPENDENT MOVEMENT OF THE
                                      MEDITINE—R7277023; PubMed-3038643; MCMahon A.P., Giebelhaus D.H., Champion T.E., Hailes T.A., Lacey S., Carritt B., Henchman S.K., Moon R.T.; Conritt B., Henchman S.K., Moon R.T.; Cham cloning, sequencing and chromosome mapping of a non-erythroid spectrin, human alpha-fodrin."; Differentiation 34:68-78(1987)
                                                                                                                                                           McMahon A.P., Giebelhaus D.H., Champion J.E., Bailes J.A., Lacey S. Carritt B., Henchman S.K., Moon R.T.;
Differentiation 34:241-241(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: LIKE ERYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
                                                                                                                                                                                                                     SEQUENCE OF 811-1529 FROM N A , VARIANT ILE-1300, AND MUTAGENESIS
                                                                                                                                                                                                                                                 MEDLINE-97146462; PubMed-8993318; Stabbeh P.E., Clanca C.B., Morrow J.S., State directed mutagenesis of alpha II spectrin at codon 1175 modulates its mu-calpain susceptibility."; Biochemistry 36·57-65(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMITARITY BELONGS TO THE SPECTRIN FAMILY.
SIMILARITY CONTAINS 2 EF-HAND CALCIUM-RINDING DOMAINS
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 23 SPECTRIN FEPFATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytoskeleton; Membrane; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
Biochem. Soc. Trans. 15:804-807(1987)
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EMBL: U83867; AA441498.1; -.
EMBL: M24773; AAA52468.1; -.
EMBL: M18627; AAA51702.1; -.
EMBL:, U26396; AAB607364.1; -.
EMHL; AF148808; AAF26672.1; -.
                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1073-1349 FROM N.A.
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InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00018; EF_HAND; 1. PROSITE; PS50002; SH3; 1.
                            SEQUENCE OF 676-1595 FROM N.A
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PRINTS; PP00452; SH3DOMAIN.
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SMAPT, SM00326, SR3, 1.
SMART, SM00150, SPEC, 20.
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                                                                                                                                                                                                                                   TISSUE-Fetal brain;
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Scientighathi, Muriche, Murinae, Pattus.
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SH3 domain; Polymorphism
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PIGGE (Rel. 14, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Spectrin alpha chain, brain (Spectrin, non erythroid alpha chain)
(Alpha II spectrin) (Fodrin alpha chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Wistar, USSUE Liver, Kalamaraki P., Gazzotti P., Cazzotti P., Cazzotti P., Cazzotti P., Cazzotti P., Cazzotti P., Cazzotti P., Cazzottional characterization of the calmodulin and calpain binding domains of rat liver alphaff spectrin."; Submitted (AUG-1946) to the EMRI/Genhank/DDBJ databases.
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N -> K (IN REF. 2).
F -> S (IN REF. 2).
V -> I (IN REF. 2).
C -> Q (ISKLE (IN REF. 2).
C -> P (IN REF. 2).
N -> S (IN REF. 3).
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A -> F (IN REF. 2).
DG -> EF (IN REF. 2).
DG -> EF (IN REF. 2).
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EF-HAND 2 (POTENTIAL).
CLEAVAGE (BY MU-CALPAIN).
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Pred. No. 1.8e+02;
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SPECTRIN 20.
SPECTRIN 21.
SPECTRIN 22.
SPECTRIN 22.
Calcium-binding, Repeat,
           SPECTRIN 1.
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SPECTRIN 3.
SPECTRIN 4.
SPECTRIN 5.
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Mammalia, Eutheria, Rodontia,
NCBI_TaxID=10116;
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2472 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                Hong W., Doyle D.; "Cloning and analysis of CDNA clones for rat kidney alpha-spectrin.";
                                                                                                                                                                                                                                                                                          CYTOSKELETON AT THE MEMBRANE (By SIMILARILY).
SURUNIT: LIKE ERYTHRONYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS
ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
                                                                                                                                                                                                                                     FUNCTION: FOREIN, WHICH SEEMS TO BE INVOLVED IN SECRETION, INTERACTS WITH CALMOULIN IN A CALCIUM-DEPENDENT MANNER AND IS
                                                  Zhou D., Ursitti J.A., Porter N.C., Randall W.R., Bloch R.J.;
"Expressional clouing of alpha fodrin from raf skeletal muscle.";
Submitted (AUG-1998) to the EMBL/ApoRank/PDRF databases.
                                                                                                                                                                                                                                                                          THUS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE
                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: HELONGS TO THE SPECTKIN FAMILY.
SIMILARITY: CONTAINS 2 EFF-HAND CALCIUM-BINDING DOMAINS.
SIMILARITY: CONTAINS 1 SHB DOMAIN.
SIMILARITY: CONTAINS 2 SPECTFIN EFFEATS.
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SPECTRIN 12.
SPECTRIN 14.
SPECTRIN 14.
SPECTRIN 16.
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SPECTRIN 19.
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SPECIRIN 5.
SPECIRIN 6.
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    Biol. Chem. 264:12758-12764(1989)

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MEDLINE-89327227; PabMod 2753883;
                                                                                                                             SEQUENCE OF 1292-2321 FROM N.A.
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PROSITE; PS00018; EF_HAND; 2.
PROSITE; PS50002; SH3; 1.
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Piam; PF00036; efband; 2.
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                                     FISSUE-Skeletal muscle;
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SMART; SM00326; SH3; 1.
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HSSP; P07751; 1AJ3.
               SHOURNCE FROM N A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galius galius (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
Archosauria: Aves: Neoquathae; Gallitormes; Phasianidae; Phasianimae;
                                                                                                                                                                                                                                                                                                       Caps
                                                                                                                                                                                  21 QOLQARNITGVI -> HADPGGEHNRSH (IN REF. 284635 MW; 08DDF01A2871278A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991 (Rei. 19, hast sequence update)
16-ocT-2001 (Rei. 40, Last annotation update)
Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wasenius V.-M., Saraste M., Knowles J., Virtanen I., Lehto V.-P., "Sequencing of the chicker non-exythroid spectrin cDNA reveals an internal repetitive structure homologous to the human erythrocyte spectrin.";
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Musacchio A., Noble M., Pauptit R., Wierenga R., Saraste M.;
Mcrystal structure of a src-homology 3 (SH3) domain.";
Nature 359:851-855(1992).
                                                                                                                                                                                                                                                61.7%; Score 37; DH 1; Length 2472;
58.3%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wasenius V.-M., Saraste M., Salven P., Eraemaa M., Holm L.,
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Pascual J., Pfuhl M., Walther D., Saraste M., Nilges M.;
"Solution structure of the spectrin repeat; a left-handed
                                                                                                                                                                                                                                                                                                  2; indels
SPECTRIN 23.
EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
                                                                                                                                     KL -> NV (IN REF. 1).
KL > NV (IN REF. 1).
QQIQARNITGVI -> HADPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lebto V.-P.; "Primary structure of the brain alpha-spectrin.";
                                                                  D > Y (IN REF. 3).
V -> L (IN REF. 1).
L -> A (IN REF. 3).
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    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1695-2153 FROM N.A.
MEDLINE-85284928; Pubmcd-4029118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHILLA
SOTACHICK STANDARD,
POTATS1,
01 AUG 1988 (Rel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell Biol, 108:79-93(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 1763-1872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBO J. 4:1425-1430(1985).
                                                                                                                                                                                                                                                                                                  7; Conservative
    2310
2347
2390
1329
11514
11972
                                                                                                                                                                                  2321
                                                                                                                                                                                                                                                                                                                                                                                      969 KELVLALYDYOF 980
                     2336 234
2379 239
1329 132
1514 151
1702 170
1971 1971
2205 220
2472 AA:
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                                                                                                                                                                                                                                                                                                                                                1 EELMLRLQDYEE 12
                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus.
NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPTANI OR SPTA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lehto V.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS.
                                                                     CONFLICT
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                     CA_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (3) MIDDLE DOMAIN (M), (4) DOMAIN BETWEEN THE MIDDLE AND C-TERMINAL DOMAIN (MC), (5) C-TERMINAL DOMAIN (M), MM AND MC DOMAINS ARE COMPOSED OF TYPICAL SPECTKIN 106 KESIDDLES REPREATS (1-8 FOR NM AND 12-19 FOR MC) AND APP HOMOLOGOUS TO EACH OTHER N, M, AND TORMAINS ARE COMPOSED FER SEQUENCES THAT LOON OTHER
                                                                                                                                                       Trave G., Lacombe J. F., Pfuhl M., Saraste M., Pastore A., Molecular mechanism of the calcium induced conformational change in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytoskeleton; Membrane; Calmodulin-bindinq; Actin-bindinq; Capping protein; Calcium-bindinq; Repeat; SH3 domain; 3D-structure. DOMAIN
                                                                                                                                                                                                                                        FUNCTION: MOPPHOLOGICALLY, SPECTPIN-LIKE PROTEINS APPEAR TO BE FELAKED TO SPECTRIN, SHOWING A FLEXIBLE PROTEINE STRUCTURE. THEY CAN HIND ACTIN BUT SERVE TO DIFFER IN THEIR CALMODULIN-BINDING ACTIVITY. IN NONERPITHROLD TISSUES, SPECTRINS, IN ASSOCIATION WITH SOME OTHER PROTEINS, MAY PLAY AN IMPORFANT
                                                                                                                                                                                                                                                                                                                                                                                                                             POLE IN MEMBERANE OPGANIZATION.
SUBUNIT: LIKE EPYTHEOCYTE SPECTPIN, THE SPECTPIN-LIKE PROTEINS
ARE CAPABLE TO FORM DIMEPS WHICH MAN FURTHER ASSOCIATE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (2) DOMAIN BETWEEN THE N-TERMINAL AND MIDDLE DOMAIN (NM), (3) MIDDLE DOMAIN (M),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: SPECTRIN-LIKE PROTEINS HAVE FIVE DOMAINS: (1) N-TERMINAL DOMAIN (N),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE SPECIFIN FAMILY. SIMILARITY: CONTAINS 1 SH3 DOMAIN.
antiparallel triple-helical coiled-coil.";
J. Mol. Hiol. 273:740-751(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X14518; CAA32662.1; -.
EMBL; X14519; CAA32663.1; ALT_SEQ.
EMBL; X02593; CAH51571.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORM TYPICAL SPECITRIN REPEATS
                                                                                          STRUCIURE BY NMP OF 2320-2403.
MEDLINE-96067121; Pubmed-7588621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR, A30122; SJCHA.
PDB, 1SHG, 31-OCT-93.
PDB, 1ACY, 15-MAC-97.
PDB, 1AJ3; 07-JUL-97.
PDB, 1TUC: 01-AUG-96.
PDH, 1TUD: 01-AUG-96.
PDH, 1HW2: 16-FEB-99.
InterPro; 1PR00204H; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001452; SH3.
InterPro; IPPA02017; Spectrin
Pfam; PF00018; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE: PSS00018; EF_HAND; 2.
PPOSITE: PSS0002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probom; pp000012; EF-hand; 1
Probom; ph000066; SH3: 1
SMART: SM00054; EFh; 2,
SMART: SM00326, SH3, 1,
SMART: SM00150; SPF0: 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00435; spectrin; 23.
PRINTS; PR00452; SH3DOMAIN.
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                                                                                                                                                                                                                     the spectrin EF-hands.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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   THE HELE TERMS AND DESCRIPTION OF THE PROPERTY AND DESCRIPTION
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                                                                                                                                                                                                                                                                                                                                         Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96077112; PubMed-7477378;
Li X.-J., Li S.-H., Sharp A.H., Nucifora H.C. Jr., Schilling G.,
Lanahan A., Worley P., Snyder S.H., Ross C.A.;
"A huntingtin associated protein enriched in brain with implications
for pathology.";
Nature 378:398-402(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukargota, Metadou: Chordata, Craniata, Vertebrata; Eufeleostomi;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                         Ö
                                                                                                                                                                                                                                                                                                                   61.7%; Score 37; DB 1; Leugth 2477; 54.3%; Pred. No. 1.8e+02; indels iive 3; Mismatches 2; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: IN CONTRAST TO HAP1, DOES NOT SEEM TO BIND TO
                                                                                                                                                                                                                                                                                                  285351 MW; AU4C8753941:6AB39 CRC64;
                                                                                                                                                              EF-HAND 1 (POTENTIAL). 
EF-HAND 2 (POTENTIAL).
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13.
15.
16.
16.
19.
21.
C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
HAPI-like protein 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
                   MIDDLE DOMAIN.
                                     MC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                            PPT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                         Conservative
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1521
1633
1739
1845
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2058
2058
2256
2352
2395
                            1026
2256
1167
1309
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1011
1017
1020
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1018 102
1021 102
2477 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCB1_1ax1D-9606;
                                             1062
1204
1310
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1522
1634
1740
1952
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2384
971
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Mond V. Gwilliam R., Fubmed-Libbasson,

RA Mond V. Gwilliam R., Fubmed-Libbasson,

RA Sqouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Hooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cromin A., Davis P., Feltwell T., Frascr A.,

Gentles S., Goble A., Hamiln N., Harris D., Hidalgo J., Hodgson G.,

RA Golroyd S., Horeby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

Androyd R., Jones L., Jones M., Leather S., McDonald S., McTean J.,

RA Jumes K., Jones L., Jones M., Leather S., McDonald S., McTean J.,

RA Jumes R., Jones L., Jones M., Leather S., McDonald S., McTean J.,

RA Hitherford K., Futter S., Saunders D., Sceger K., Sharp S.,

RA Hitherford K., Futter S., Saunders D., Sceger K., Sharp S.,

RA Skelton J., Simmonds M., Squares K., Sharp S.,

RA Skelton J., Valckaert G., Aert R., Robben J., Grymonprez B.,

RA Goddward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Gobel C., Puchs M., Fritze C., Holzer E., Mocstl D., Hilbert H.,

RA Gollean L., Vanstreris E., Riende H., Reinhardt R., Pohl T.M.,

RA Gollean A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,

RA Lucas M., Rechet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Lucas M., Rechet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Lucas M., Rechet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Lucas M., Rechet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Lucas M., Revuella J.L., Moreno S., Armstrong J., Porsburg S.L.,

RA Hornywski G.V., Ussery D., Barrell B.G., Nurse P.,

Miller H., Raylland R., Schlicosaccharomyces pombe.";

Miller H. H., Raylland R., Salland R., Nurse P.,

Miller R., Raylland R., Salland R., Nurse P.,

Miller R., Raylland R., Schlicosaccharomyces pombe.";
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-oct:2001 (Rcl. 40, Created)
16-oct:2001 (Rcl. 40, Last sequence update)
15-uUN-2002 (Rcl. 41, Last annotation update)
Probable ethanolamine-phosphate cylidylyltranslerase (EC 2.7.7.14)
(Phosphorylethanolamine transferase) (CTP:phosphoethanolamine
                                                                                                                                                                                                                                                                                ...
                                                                                                                                                                                                                                   Secore 36; DB 1; Length 320;
                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                     320 AA 37202 MW. FP404RIRER6A0EE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi: Ascomycota, Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                                                                                                                                                                                                3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                          320
                                                                                              Genew; HGNC:4812; HAP1.
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                                                                      FMR1 - 1148471 -
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This YWYMS-PWOT LETTY is E-FYTIGHT. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

PATHWAY: PHOSPHOLIPID BIOSYNTHESIS; CDP-ETHANOLAMINE SYNTHESIS;

!- SIMILARITY: BELONGS TO THE CYTIDYLYLTRANSFERASE FAMILY.

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                                                                                                                                         InterPro; IPR04821; Cyt_tran_rel.
InterPro; IPR04822; Cyt.dylylyltrans1.
InterPro; IPR0467; Cyt.dylylyltrans1.
IIGRFAMS; TIGR00125, Cyt_tran_rel.
ITGRFAMS; TIGR00125, Cyt_tran_rel.
Iransferase; Neleotidyltransferase; Phospholipid biosynthesis.
DOMAIN
I 182
CATALYTIC (POTENTIAL).
SEQUENCE: 365 AA; 41555 MW; ACDH6A974AHH4734 CRC64;
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                                                                                                                                                                                                                                                                                                                       60.0%; Score 36; DB 1; Length 365;
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                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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18.4857 secs
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                                                                                                                                                                                                                                                                                                                                                58.3%;
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                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 58.3
Matches 7; Conservative
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